FIG. 1

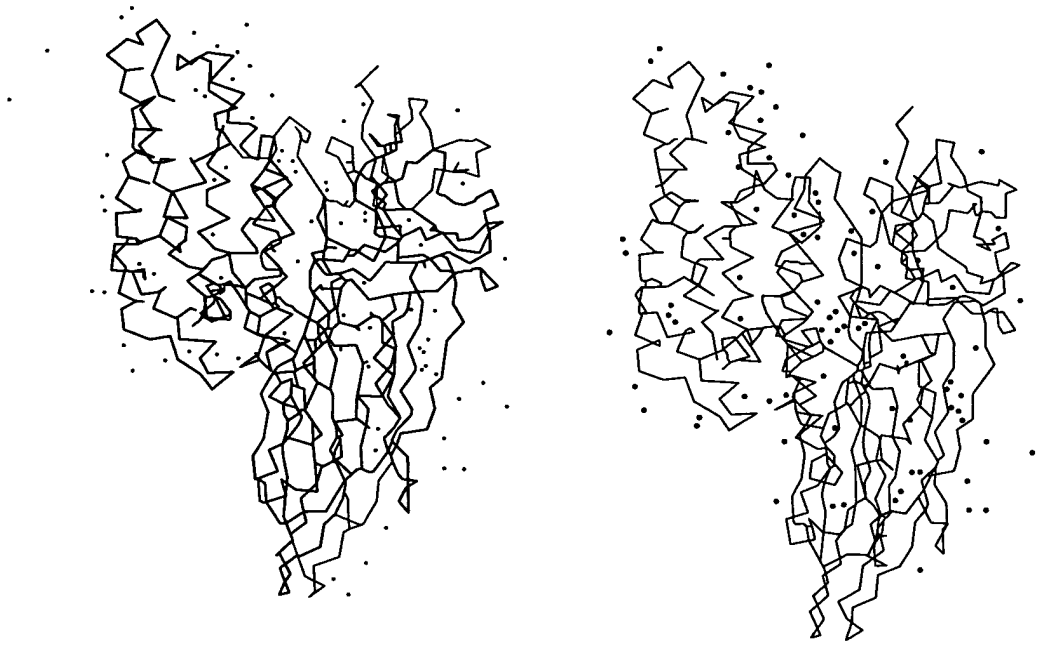

FIG. 2

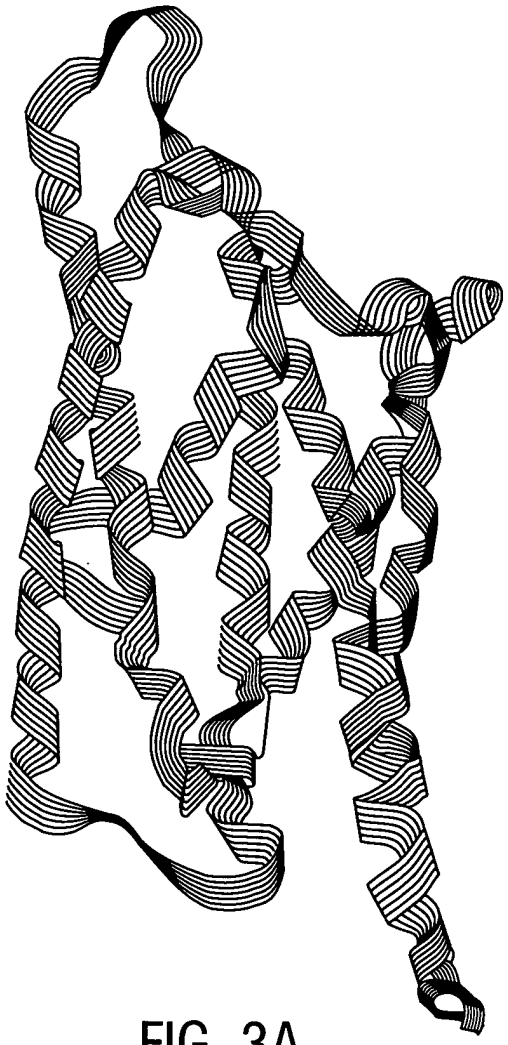

FIG. 3A

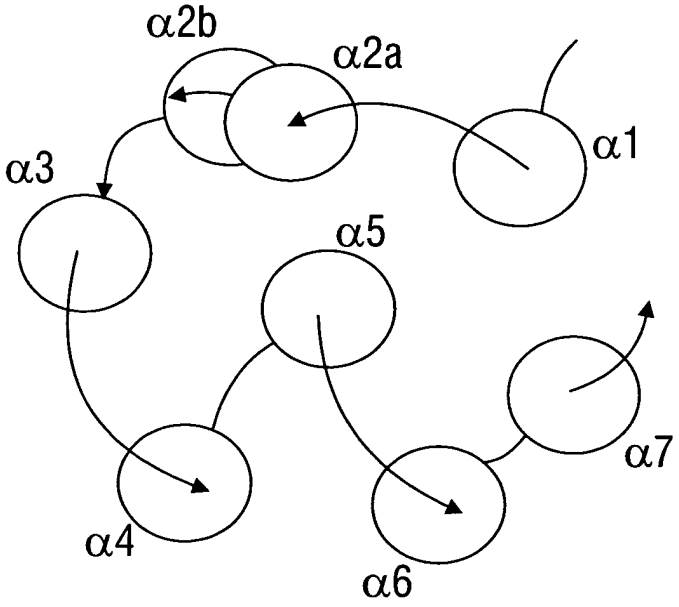

FIG. 3B

alpha helix	Amino acid Residues
α1	63-79
α2a	85-98
α2b	105-118
α3	124-153
α4	161-186
α5	194-215
α6	223-255
α7	260-286

FIG. 4

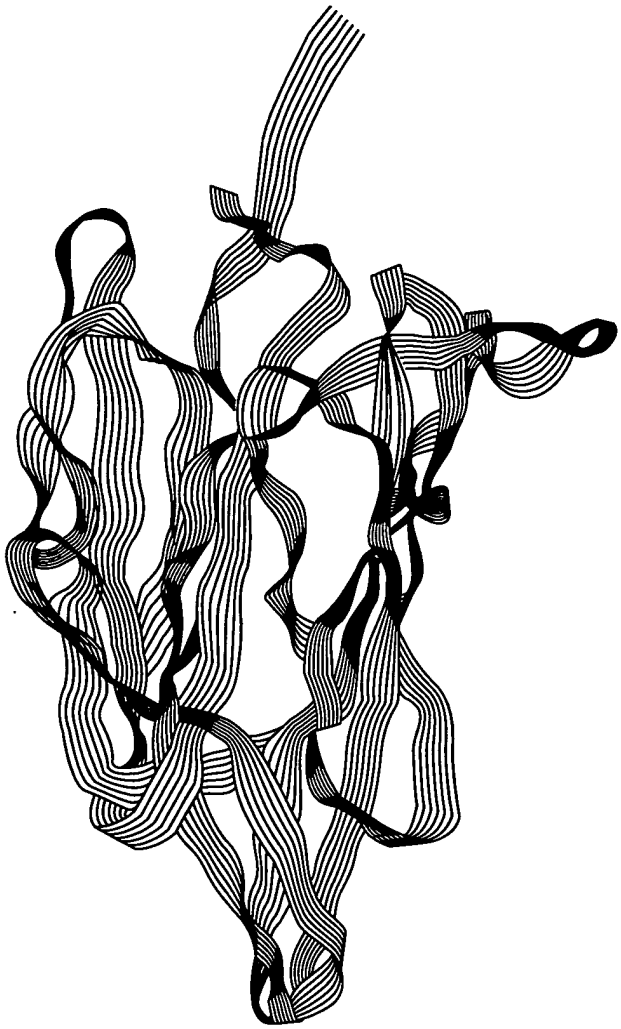

FIG. 5A

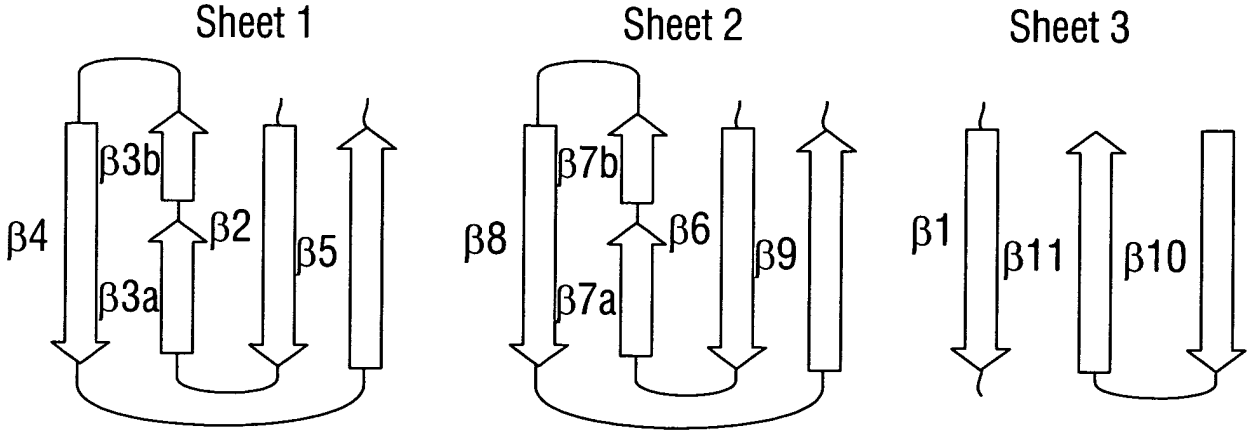
Sheet 1
Sheet 2
Sheet 3
β4
β3b
β3a
β2
β5
β8
β7b
β7a
β6
β9
β1
β11
β10

FIG. 5B

Sheet 1

β Strand	Amino Acid Residue
β2	339-350
β3a	256-360
β3b	362-368
β4	375-379
β5	390-395

Sheet 2

β Strand	Amino Acid Residue
β6	402-412
β7a	416-419
β7b	423-430
β8	435-442
β9	452-456

Sheet 3

β Strand	Amino Acid Residue
β1	296-306
β10	472-483
β11	492-498

FIG. 6

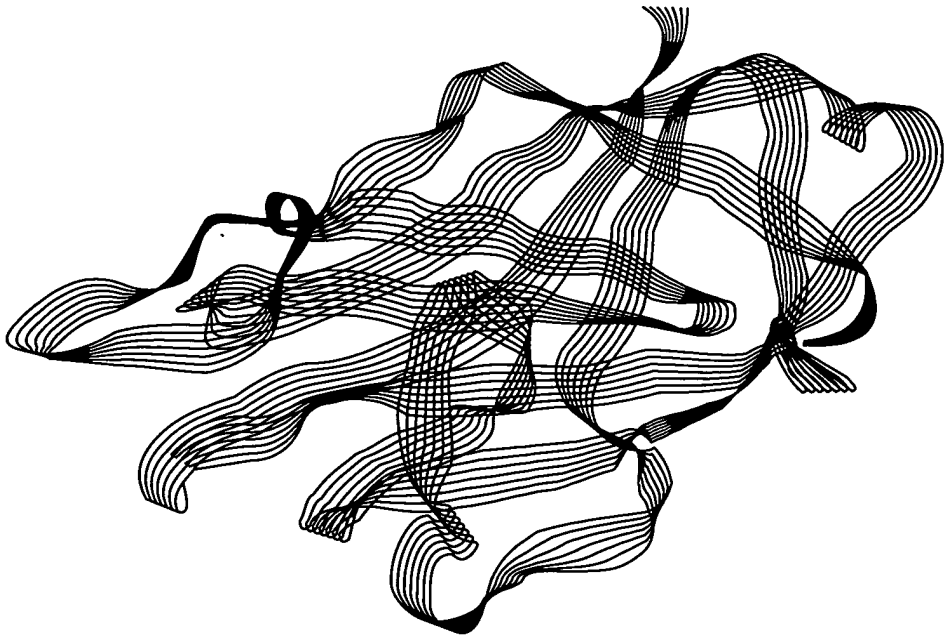

FIG. 7A

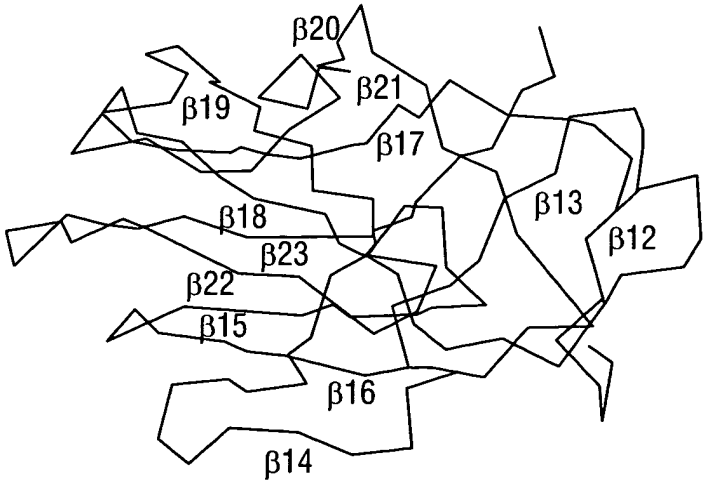

FIG. 7B

Strand Number	Amino Acid Residues
β12	505-509
β13	512-515
β14	522-528
β15	539-544
β16	550-557
β17	563-574
β18	578-584
β19	590-596
β20	609-614
β21	616-619
β22	626-636
β23	638-650

FIG. 8

FIG. 9A

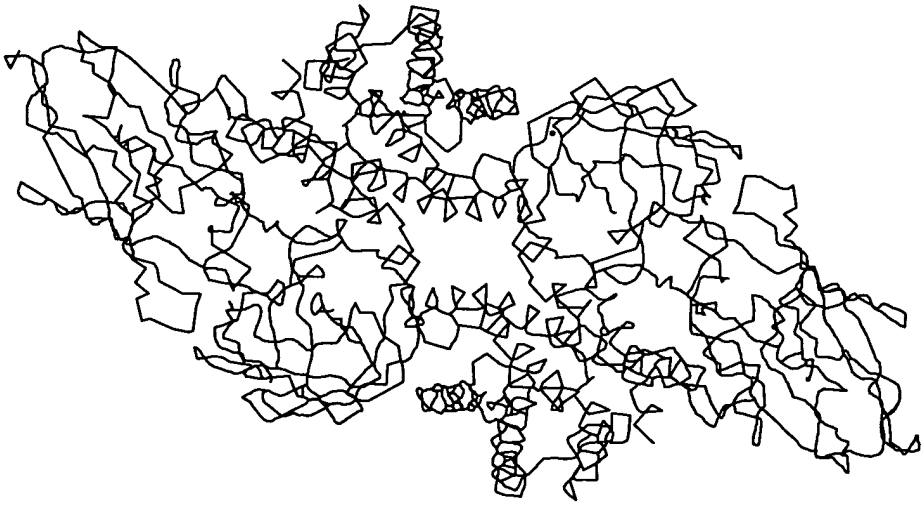

FIG. 9B

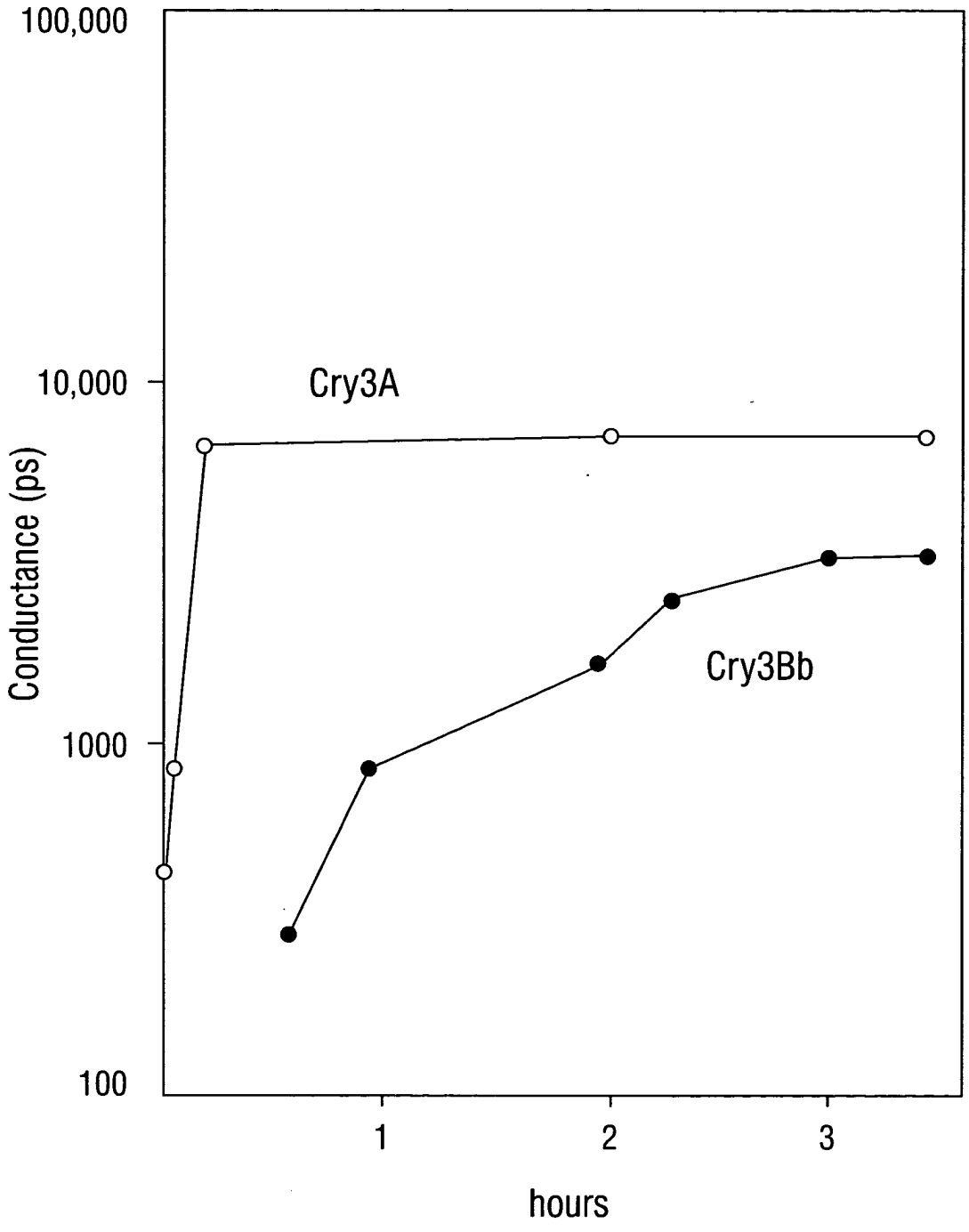
100,000
10,000
1000
100
Conductance (ps)
Cry3A
Cry3Bb
1
2
3
hours

FIG. 10

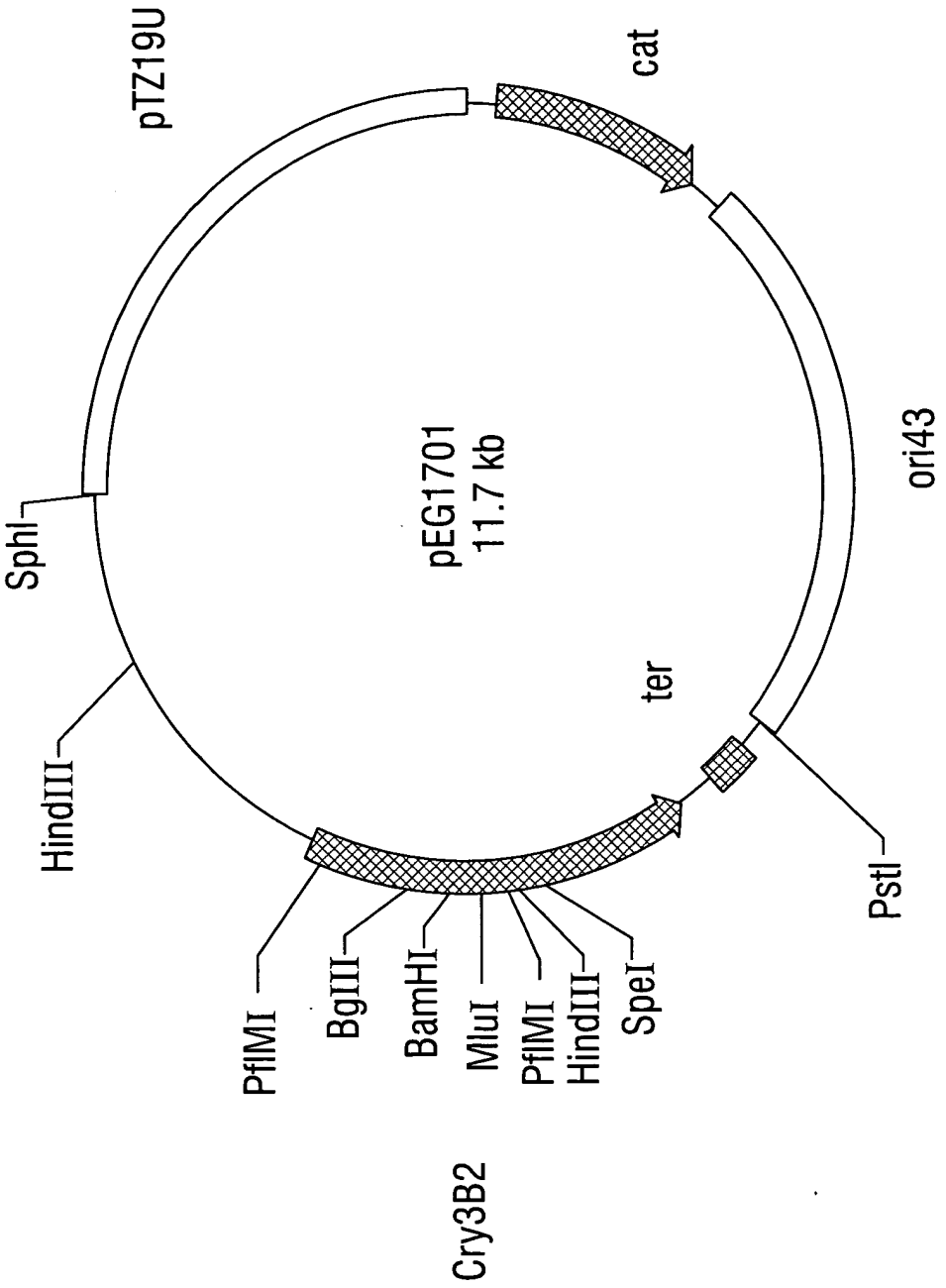
pTZ19U
cat
pEG1701
11.7 kb
ori43
ter
SphI
HindIII
PflMI
BglII
BamHI
MluI
PflMI
HindIII
SpeI
PstI
Cry3B2

FIG. 11

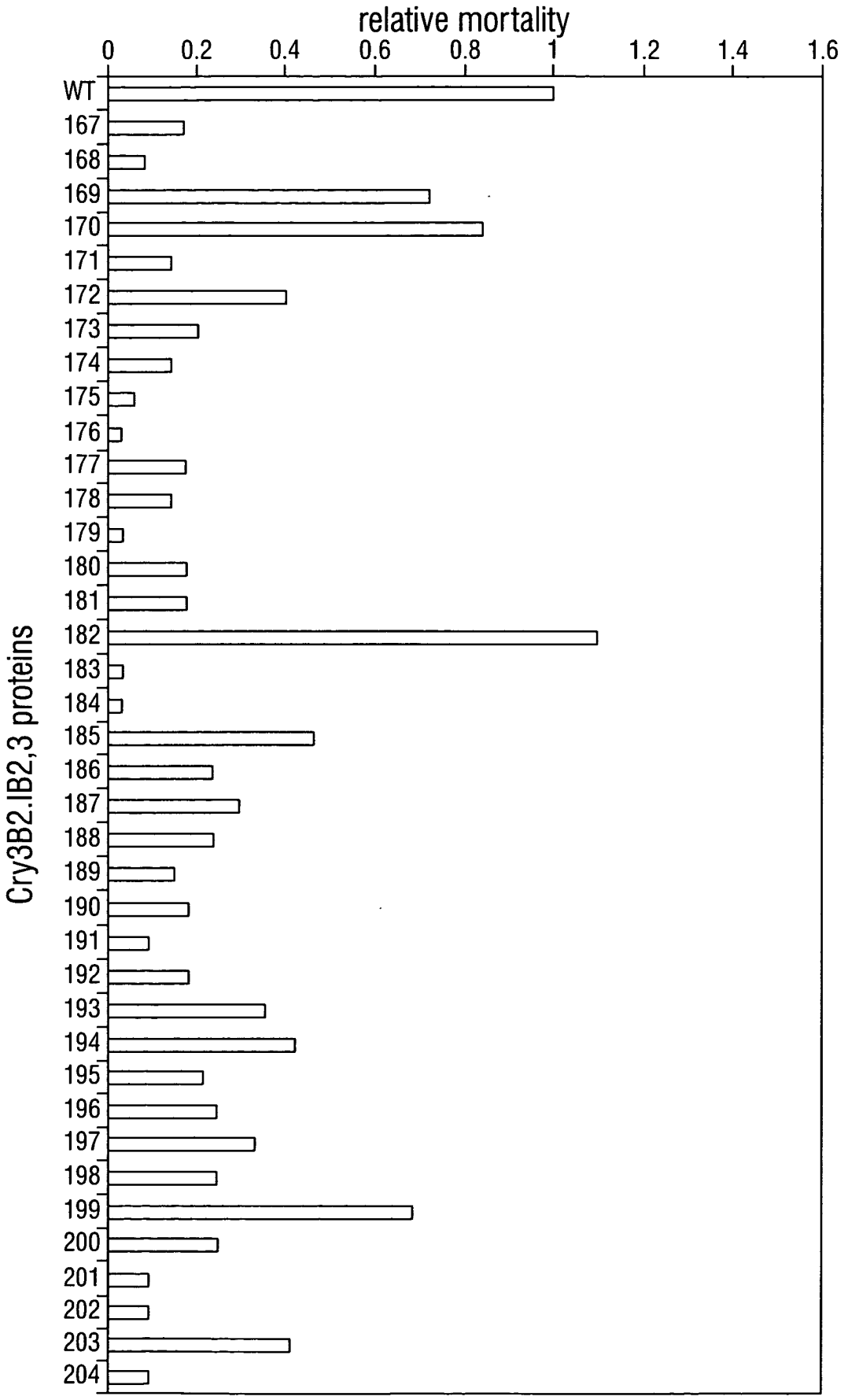
relative mortality
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
Cry3B2.IB2,3 proteins
WT
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204

FIG. 12

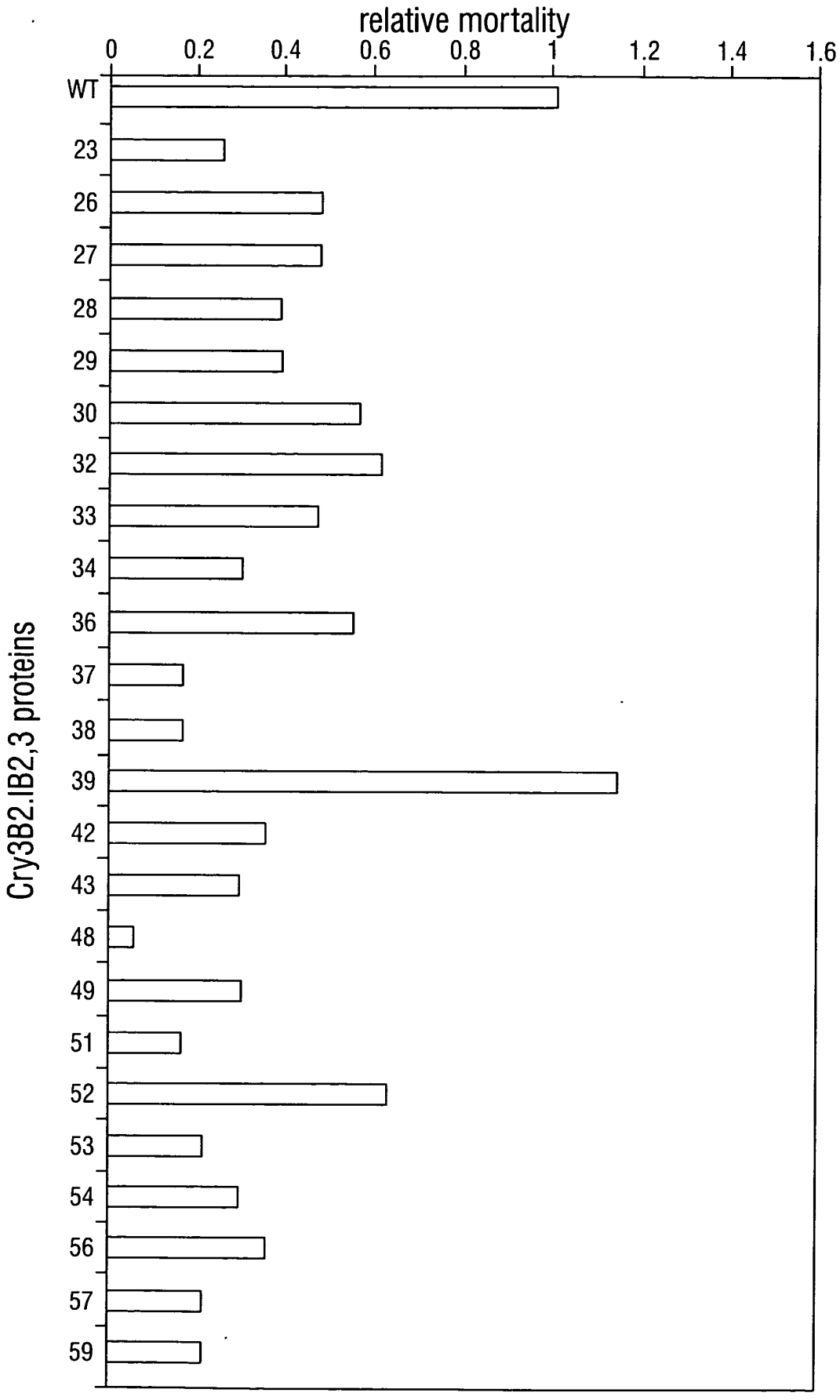
relative mortality
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
Cry3B2.IB2,3 proteins
WT
23
26
27
28
29
30
32
33
34
36
37
38
39
42
43
48
49
51
52
53
54
56
57
59

FIG. 13

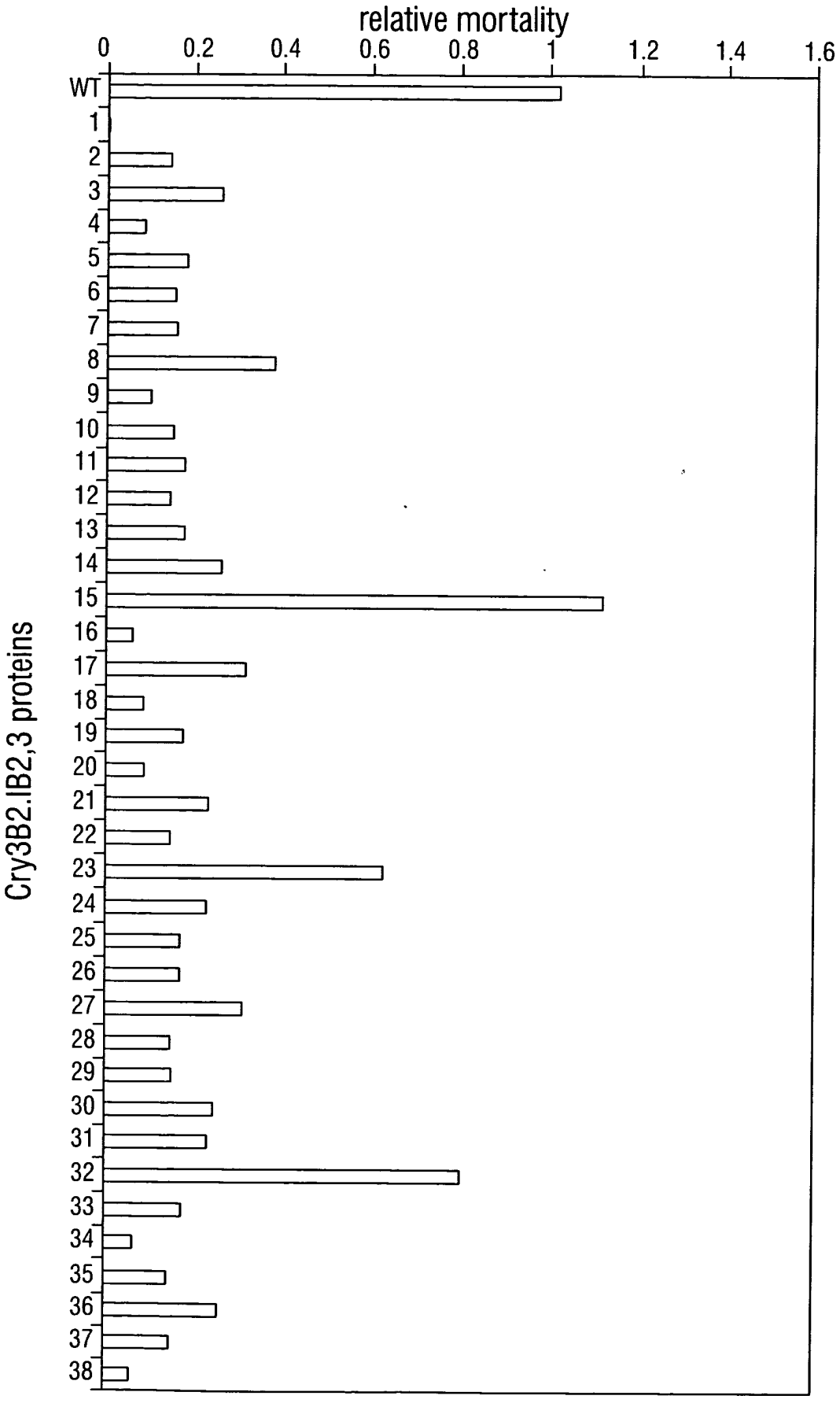
relative mortality
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
Cry3B2.IB2,3 proteins
WT
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38

FIG. 14

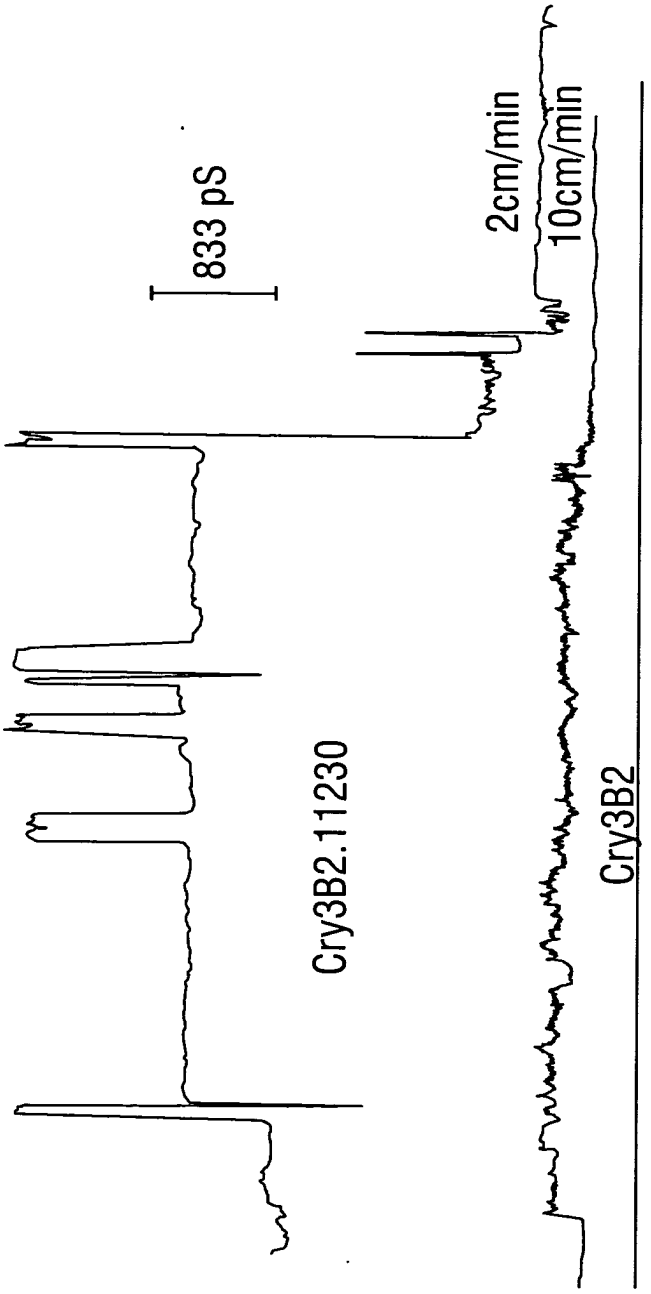

FIG. 15

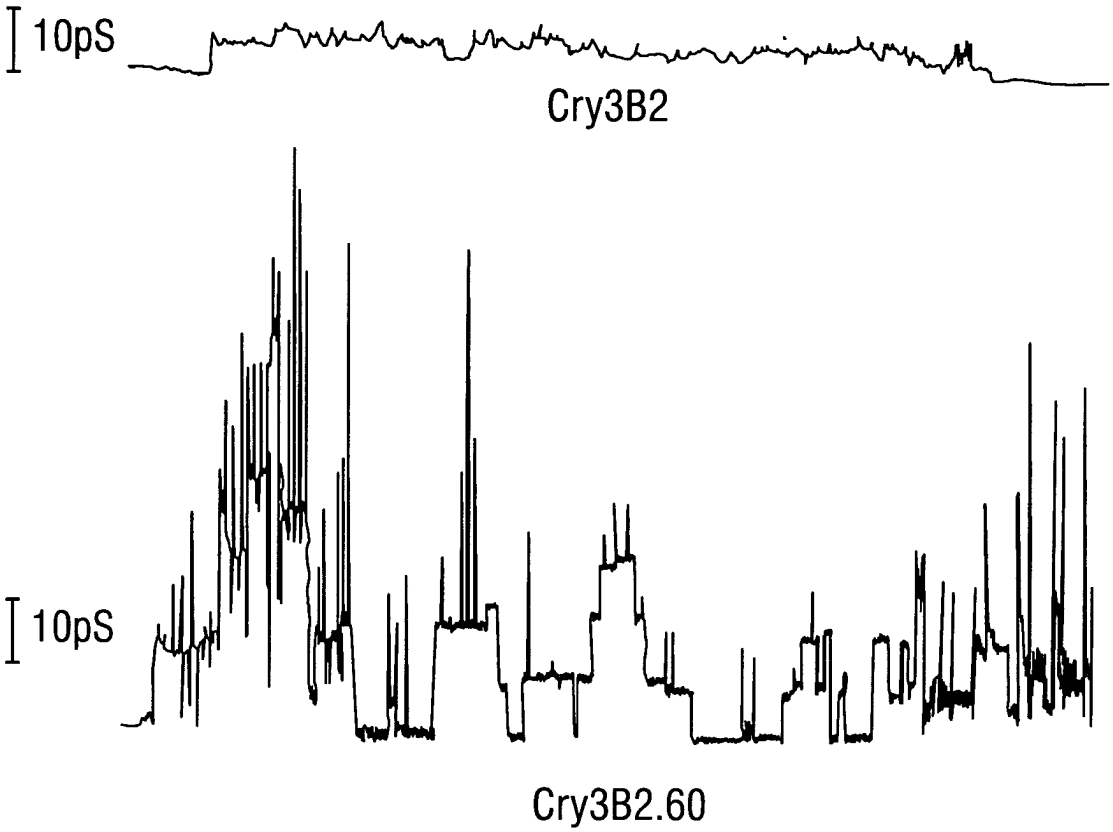

FIG. 16

ALIGNMENT OF CRY3 SEQUENCES

(Numbered according to Cry3BB)
(alpha helices underlined, beta sheets marked with +++'s)

```
                1         10         20         30         40
CRY3C:          MNPNNRSEHDTIKATENNEVSNNHAQYPLADTP--TLEELNY
CRYCBB2:        MNPNNRSEHDTIKVTPNSELPTNHNQYPLADNPNSTLEELNY
CRY3BB:         MNPNNRSEHDTIKVTPNSELQTNHNQYPLADNPNSTLEELNY
CRY3BA:  MIRMGGRKMNPNNRSEYDTIKVTPNSELPTNHNQYPLADNPNSTLEELNY
CRY3A:   MIRKGGRKMNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNY

                50         60         70         80         90
CRY3C:   KEFLRRTTDNNVEALDSSTTKDAIQKGISIIGDLLGVVGFPYGGALVSFY
CRYCBB2: KEFLRMTEDSSTEVLDNSTVKDAVGTGISVVGQILGVVGVPFAGALTSFY
CRY3BB:  KEFLRMTEDSSTEVLDNSTVKDAVGTGISVVGQILGVVGVPFAGALTSFY
CRY3BA:  KEFLRMTADNSTEVLDSSTVKDAVGTGISVVGQILGVVGVPFAGALTSFY
CRY3A:   KEFLRMTADNNTEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFY

               100        110        120        130        140
CRY3C:   TNLLNTIWPGE-DPLKAFMQQVEALIDQKIADYAKDKATAELQGLKNVFK
CRY3BB2: QSFLDTIWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAELQGLQNNFE
CRY3BB:  QSFLNTIWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAELQGLQNNFE
CRY3BA:  QSFLNAIWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAELQGLQNNFE
CRY3A:   TNFLNTIWPSE-DPWKAFMEQVEALMDQKIADYAKNKALAELQGLQNNVE

               150        160        170        180        190
CRY3C:   DYVSALDSWDKTPLTLRDGRSQGRIRELFSQAESHFRRSMPSFAVSGYEV
CRY3BB2: DYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEV
CRY3BB:  DYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEV
CRY3BA:  DYVNALDSWKKAPVNLRSRRSQDRIRELFSQAESHFRNSMPSFAVSKFEV
CRY3A:   DYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAISGYEV
```

FIG. 17A

```
                200       210       220       230       240
CRY3C:     LFLPTYAQAANTHLLLLKDAQIYGTDWGYSTDDLNEFHTKQKDLTIEYTN
CRY3BB2:   LFLPTYAQAANTHLLLLKDAQVFGEEWGYSSEDVAEFYHRQLKLTQQYTD
CRY3BB:    LFLPTYAQAANTHLLLLKDAQVFGEEWGYSSEDVAEFYHRQLKLTQQYTD
CRY3BA:    LFLPTYAQAANTHLLLLKDAQVFGEEWGYSSEDIAEFYQRQLKLTQQYTD
CRY3A:     LFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYTD

                250       260       270       280       290
CRY3C:     HCAKWYKAGLDKLRGSTYEEWVKFNRYRREMTLTVLDLITLFPLYDVRTY
CRYS3BB2:  HCVNWYNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFYDVRLY
CRY3BB:    HCVNWYNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFYDIRLY
CRY3BA:    HCVNWYNVGLNSLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFYDVRLY
CRY3A:     HCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLY

                300       310       320       330       340
CRY3C:     TKGVKTELTRDVLTDPIVAVNNMNGYGTTFSNIENYIRKPHLFDYLHAIQ
CRY3BB2:   SKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLQGIE
CRY3BB:    SKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLQGIE
CRY3BA:    SKGVKTELTRDIFTDPIFTLNALQEYGPTFSSIENSIRKPHLFDYLRGIE
CRY3A:     PKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQ
              ++++++++++                                 ++++

                350       360       370       380       390
CRY3C:     FHSRLQPGYFGTDSFNYWSGNYVSTRSSIGSDEIIRSPFYGNKSTLDVQN
CRY3BB2:   FHTRLQPGYSGKDSFNYWSGNYVETRPSIGSSKTITSPFYGDKSTEPVQK
CRY3BB:    FHTRLQPGYFGKDSFNYWSGNYVETRPSIGSSKTITSPFYGDKSTEPVQK
CRY3BA:    FHTRLRPGYSGKDSFNYWSGNYVETRPSIGSNDTITSPFYGDKSIEPIQK
CRY3A:     FHTRFQPGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQN
           ++++++++      +++++ +++++++       +++++           +++

                400       410             420       430
CRY3C:     LEFNGEKVFRAVANGNLAVWPVGTGGTKIHSGVTKVQFSQYNDRKDEVRT
CRY3BB2:   LSFDGQKVYRTIANTDVAAWPNG----KIYFGVTKVDFSQYDDQKNETST
CRY3BB:    LSFDGQKVYRTIANTDVAAWPNG----KVYLGVTKVDFSQYDDQKNETST
CRY3BA:    LSFDGQKVYRTIANTDIAAFPDG----KIYFGVTKVDFSQYDDQKNETST
CRY3A:     LEFNGEKVYRAVANTNLAVWPSA-----VYSGVTKVEFSQYNDQTDEAST
           +++       ++++++++++        ++++    ++++++++     ++++
```

FIG. 17B

```
          440        450        460        470        480
CRY3C:    QTYDSKRNVGGIV-FDSIDQLPPITTDESLEKAYSHQLNYVRCFLLQGGR
CRY3BB2:  QTYDSKRNNGHVGAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR
CRY3BB:   QTYDSKRNNGHVSAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR
CRY3BA:   QTYDSKRYNGYLGAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR
CRY3A:    QTYDSKRNVGAVS-WDSIDQLPPETTDEPLEKGYSHQLNYVMCFLMQGSR
          ++++         +++++                      +++++++

          490       500        510        520        530
CRY3C:    GIIPVFTWTHKSVDFYNTLDSEKITQIPFVKAFILVNSTSVVAGPGFTGG
CRY3BB2:  GTIPFFTWTHRSVDFFNTIDAEKITQLPVVKAYALSSGASIIEGPGFTGG
CRY3BB:   GTIPFFTWTHRSVDFFNTIDAEKITQLPVVKAYALSSGASIIEGPGFTGG
CRY3BA:   GTIPFFTWTHRSVDFFNTIDAEKITQLPVVKAYALSSGASIIEGPGFTGG
CRY3A:    GTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGG
             +++++++      +++++  ++++      +++++++

          540        550       560        570        580
CRY3C:    DII-KCT-NGSGLTLYVTPAPDLTYSKTYKIRIRYASTSQVRFGIDLGSY
CRY3BB2:  NLLFLKESSNSIAKFKVTL-NSAALLQRYRVRIRYASTTNLRLFVQNSNN
CRY3BB:   NLLFLKESSNSIAKFKVTL-NSAALLQRYRVRIRYASTTNLRLFVQNSNN
CRY3BA:   NLLFLKESSNSIAKFKVTL-NSAALLQRYRVRIRYASTTNLRLFVQNSNN
CRY3A:    DII-QCTENGSAATIYVTPD--VSYSQKYRARIHYASTSQITFTLSLDGA
          ++++++     ++++++++      ++++++++++++   +++++++

          590        600        610        620        630
CRY3C:    THSISYFDKTMDKGNTLTYNSFNLSSVSRPIEISG-GNKIGVSVGGIGSG
CRY3BB2:  DFIVIYINKTMNIDDDLTYQTFDLATTNSNMGFSGDTNELIIGAESFVSN
CRY3BB:   DFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN
CRY3BA:   DFLVIYINKTMNIDGDLTYQTFDFATSNSNMGFSGDTNDFIIGAESFVSN
CRY3A:    PFNQYYFDKTINKGDTLTYNSFNLASFSTPFELSG--NNLQIGVTGLSAG
            +++++++           +++++++ ++++      ++++++++++

          640        650
CRY3C:    DEVYIDKIEFIPMD
CRY3BB2:  EKIYIDKIEFIPVQL
CRY3BB:   EKIYIDKIEFIPVQL
CRY3BA:   EKIYIDKIEFIPVQ
CRY3A:    DKVYIDKIEFIPVN
          ++++++++++++
```

FIG. 17C